



SEQUENCE LISTING

<110> Sauter, Margret M
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
CONDITIONS

<130> 2283/201

<140> 09/785,738

<141> 2001-02-16

<150> 60/183,572

<151> 2000-02-18

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 872

<212> DNA

<213> Rice

<220>

<221> CDS

<222> (69)..(668)

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Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
1 5 10
gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
15 20 25 30
cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
35 40 45
gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
50 55 60
ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
65 70 75
gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350
Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
80 85 90
ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398
Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu
95 100 105 110

gaa	ggg	agt	gga	tac	ttt	gat	gtg	aga	gac	caa	aat	gat	cag	tgg	att	446
Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Gln	Asn	Asp	Gln	Trp	Ile	
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cgt	ata	gca	ctg	aag	aaa	gga	ggc	atg	att	gtt	ctg	cct	gca	ggg	atg	494
Arg	Ile	Ala	Leu	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Met	
			130					135					140			
tac	cac	cgc	ttt	acg	ttg	gac	acc	gac	aac	tat	atc	aag	gca	atg	cga	542
Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	
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ctg	ttt	gtt	ggc	gat	cct	gtt	tgg	aca	ccc	tac	aac	cgt	ccc	cat	gac	590
Leu	Phe	Val	Gly	Asp	Pro	Val	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	
	160					165					170					
cat	ctt	cct	gca	aga	aag	gag	ttt	ttg	gct	aaa	ctt	ctc	aag	tca	gaa	638
His	Leu	Pro	Ala	Arg	Lys	Glu	Phe	Leu	Ala	Lys	Leu	Leu	Lys	Ser	Glu	
175					180					185					190	
ggg	gaa	aat	caa	gca	gtt	gaa	ggc	ttc	tga	ggg	ttt	gtt	ggg	ctc	gtc	688
Gly	Glu	Asn	Gln	Ala	Val	Glu	Gly	Phe								
			195					200								
actg	cggttc	tatatt	caac	ctga	ataaga	tgtg	ctatag	caat	gtaaat	ttag	cacagt					748
ggct	atggtc	gccact	cacc	aact	tgaagt	gaaag	attta	atgatt	ttttg	ttaatt	ctta					808
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			20					25					30			
Pro	Lys	Glu	Phe	Ile	Pro	Val	Asp	Lys	Leu	Thr	Glu	Leu	Gly	Val	Ile	
		35					40					45				
Ser	Trp	Arg	Leu	Asn	Pro	Asp	Asn	Trp	Glu	Asn	Cys	Glu	Asn	Leu	Lys	
	50					55				60						
Arg	Ile	Arg	Glu	Ala	Arg	Gly	Tyr	Ser	Tyr	Val	Asp	Ile	Cys	Asp	Val	
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Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Thr	Lys	Ile	Lys	Ser	Phe	Phe	
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Glu	Glu	His	Leu	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	
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Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Gln	Asn	Asp	Gln	Trp	Ile	Arg	Ile	
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gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
15 20 25

cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
30 35 40

gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat 315
Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
45 50 55

gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg 363
Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
60 65 70 75

gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag 411
Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
80 85 90

ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc 459
Leu Lys Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
95 100 105

tat	tgt	ctt	gag	gga	agt	gga	tac	ttc	gat	gtc	agg	gac	caa	aat	gat	507
Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Gln	Asn	Asp	
		110					115					120				

cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct 555
Gln Trp Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
125 130 135

gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag 603
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<213> Rice

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Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser Glu Leu Gly Ile Leu
          35          40          45
Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
          50          55          60
Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
          65          70          75          80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
          85          90          95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
          100          105          110
Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
          115          120          125
Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
          130          135          140
Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
          145          150          155          160
Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
          165          170          175
Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile Asn Arg Gly Gly Thr
          180          185          190
Gln Ala Val Glu Ala Arg
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<210> 5
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<212> DNA
<213> Tomato

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<220>

<221> CDS

<222> (1) .. (591)

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aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt	96
Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe	
20 25 30	
gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt	144
Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu	
35 40 45	
gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa	192
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu	
50 55 60	
gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa	240
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys	
65 70 75 80	
cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg	288
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu	
85 90 95	
cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt	336
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe	
100 105 110	
gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa	384
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys	
115 120 125	
ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt	432
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu	
130 135 140	
gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca	480
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro	
145 150 155 160	
att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa	528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln	
165 170 175	
gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt	576
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val	
180 185 190	
aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt	631
Asn Ala Ala	
195	
aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt	691
aatgttgat tgtggcacta aataaatcac cccctatggg agattgattg tttatatgca	751

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774

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Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
35 40 45
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
50 55 60
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65 70 75 80
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
85 90 95
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
100 105 110
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145 150 155 160
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
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Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
180 185 190
Asn Ala Ala Ala
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<212> DNA
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<220>
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gat cag cgg cta ccg cac cag aag aac cca ccg gag ttt gtt tca gtg 95
Asp Gln Arg Leu Pro His Gln Lys Asn Pro Pro Glu Phe Val Ser Val
20 25 30
gag aaa tta gca gta atc gga gtt tta tac tgg aaa ttg aac cct aat 143
Glu Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn
35 40 45
gat tac gag aac gat gaa gaa ttg aaa aaa att cgt caa agt aga ggc 191

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		50					55					60					
tac	agc	tac	atg	gac	ttg	ctg	gat	ttg	tgc	cct	gag	aag	gtg	gat	aac	239	
Tyr	Ser	Tyr	Met	Asp	Leu	Leu	Asp	Leu	Cys	Pro	Glu	Lys	Val	Asp	Asn		
	65					70				75							
tat	gag	cag	aag	ttg	aaa	aat	ttc	tat	acg	gag	cac	ata	cac	gca	gat	287	
Tyr	Glu	Gln	Lys	Leu	Lys	Asn	Phe	Tyr	Thr	Glu	His	Ile	His	Ala	Asp		
	80				85				90						95		
gag	gag	ata	cgt	tac	tgt	ctg	gaa	ggg	agt	gga	tat	ttt	gat	gtg	aga	335	
Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg		
			100						105					110			
gac	aag	gat	gat	cgc	tgg	att	cgc	atc	tgg	atg	aag	gcc	ggt	gat	atg	383	
Asp	Lys	Asp	Asp	Arg	Trp	Ile	Arg	Ile	Trp	Met	Lys	Ala	Gly	Asp	Met		
		115					120						125				
att	gtc	ttg	cct	gct	ggg	att	tac	cac	cgg	ttc	acc	cta	gat	act	gat	431	
Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp		
		130					135					140					
aac	tat	gtc	aag	ttg	atg	agg	ttg	ttt	gtg	gga	gag	ccg	gtg	tgg	acg	479	
Asn	Tyr	Val	Lys	Leu	Met	Arg	Leu	Phe	Val	Gly	Glu	Pro	Val	Trp	Thr		
	145					150				155							
cct	tac	aat	cga	cca	caa	gaa	gat	cat	cca	gca	agg	aag	gag	tac	atc	527	
Pro	Tyr	Asn	Arg	Pro	Gln	Glu	Asp	His	Pro	Ala	Arg	Lys	Glu	Tyr	Ile		
	160				165				170						175		
aag	agt	gtt	act	gaa	aga	gta	gga	gtg	cct	ctt	aca	gca	cac	taa		572	
Lys	Ser	Val	Thr	Glu	Arg	Val	Gly	Val	Pro	Leu	Thr	Ala	His				
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<212> PRT

<213> Tomato

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Gln	Arg	Leu	Pro	His	Gln	Lys	Asn	Pro	Pro	Glu	Phe	Val	Ser	Val	Glu		
		20						25					30				
Lys	Leu	Ala	Val	Ile	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asn	Pro	Asn	Asp		
	35						40					45					
Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Gln	Ser	Arg	Gly	Tyr		
	50					55				60							
Ser	Tyr	Met	Asp	Leu	Leu	Asp	Leu	Cys	Pro	Glu	Lys	Val	Asp	Asn	Tyr		
	65				70				75					80			
Glu	Gln	Lys	Leu	Lys	Asn	Phe	Tyr	Thr	Glu	His	Ile	His	Ala	Asp	Glu		
			85					90						95			
Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp		
		100					105					110					
Lys	Asp	Asp	Arg	Trp	Ile	Arg	Ile	Trp	Met	Lys	Ala	Gly	Asp	Met	Ile		
	115					120						125					
Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn		

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<212> DNA
<213> Soybean
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Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
10 15 20

gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg 148
Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu
25 30 35

gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat 196
Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
40 45 50 55

aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt 244
Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
60 65 70

tac	acc	tac	atg	gat	gtt	tgt	gag	gtc	tgc	cca	gaa	aag	ttg	cca	aat	292
Tyr	Thr	Tyr	Met	Asp	Val	Cys	Glu	Val	Cys	Pro	Glu	Lys	Leu	Pro	Asn	
			75					80					85			

tat	gaa	cag	aaa	atc	aaa	agc	ttc	ttt	gaa	gag	cat	ctt	cac	act	gat	340
Tyr	Glu	Gln	Lys	Ile	Lys	Ser	Phe	Phe	Glu	Glu	His	Leu	His	Thr	Asp	
		90					95					100				

gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg 388
Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
105 110 115

gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg 436
Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120 125 130 135

atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc 484
Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser
140 145 150

aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act 532


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Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
      155                      160                      165

cca tac aat cgt cca aat gac cat ctc cct gca aga caa caa tat gtc 580
Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val
      170                      175                      180

aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc 628
Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
      185                      190                      195

gcg taa gatctgggttc tgcctaataca tagtaccaca tgaaaaggac caagactttg 684
Ala
200

ttgctaaagt aagggtttgaa aaaaagaaaa taatggtgtc tttaaataaaa gggctcctggc 744

ttgttatgcc ttgatgtacc ctgcgcagtg tttttgttgc ctgtccctgt ataaagattg 804

cattgtatta ttattagaat tgggtacaga ataaacataa gcataagtta gcatgctgat 864

gtatatattat gtaaaaaaaaa ataaa 889

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<210> 10
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 <213> Soybean

<400> 10

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      20          25          30
Pro Lys Glu Phe Val Ser Leu Asp Gln Leu Ala Glu Leu Gly Val Leu
      35          40          45
Ser Trp Lys Leu Asp Ala Asp Asn His Glu Asn Asp Pro Glu Leu Lys
      50          55          60
Lys Ile Arg Glu Glu Arg Gly Tyr Thr Tyr Met Asp Val Cys Glu Val
      65          70          75          80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe
      85          90          95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly
      100          105          110
Ser Gly Tyr Phe Asp Val Arg Asp Arg Asn Glu Ala Trp Ile Arg Val
      115          120          125
Trp Val Lys Lys Gly Gly Met Ile Ile Leu Pro Ala Gly Ile Tyr His
      130          135          140
Arg Phe Thr Leu Asp Glu Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe
      145          150          155          160
Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro Asn Asp His Leu
      165          170          175
Pro Ala Arg Gln Gln Tyr Val Lys Asp Phe Val Glu Lys Asp Val Ser
      180          185          190
Ser His Ala Val Asp Ala Thr Ala
      195          200

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<211> 933
<212> DNA
<213> Cotton

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<222> (33)..(635)

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Lys Arg Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
      10                               15                               20

gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg 149
Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
      25                               30                               35

gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat 197
Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
      40                               45                               50                               55

aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt 245
Asn Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
      60                               65                               70

tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat 293
Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
      75                               80                               85

tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat 341
Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
      90                               95                               100

gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg 389
Glu Glu Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
      105                               110                               115

gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg 437
Asp His Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
      120                               125                               130                               135

ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac 485
Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
      140                               145                               150

aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act 533
Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
      155                               160                               165

ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc 581
Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
      170                               175                               180

aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629
Lys Asn Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
      185                               190                               195

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gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg ccgcataaaa 685
Ala
200

tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggtaata 745
aataagtcta ggcttgtctg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805
ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtattt ctacatttta 865
tgtgcttact accagattgg ctcttaataa tcaaagttta cataatatac atttcgtcga 925
cgcgggccg 933

<210> 12
<211> 200
<212> PRT
<213> Cotton

<400> 12
Met Thr Met Gly Ser Ala Asp Lys Arg Glu Glu Val Ile Gln Ala Trp
1 5 10 15
Tyr Met Asp Asp Ser Asp Glu Asp Gln Arg Leu Pro His His Arg Glu
20 25 30
Pro Lys Glu Tyr Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu
35 40 45
Ser Trp Arg Leu Asp Ala Asp Asn Tyr Glu Asn Asp Glu Glu Leu Lys
50 55 60
Lys Ile Arg Glu Glu Arg Gly Tyr Ser Tyr Met Asp Phe Cys Glu Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe
85 90 95
Glu Glu His Ile His Thr Asp Glu Glu Ile Arg Tyr Cys Val Ala Gly
100 105 110
Ser Gly Tyr Phe Asp Val Arg Asp His Asn Asp Lys Trp Ile Arg Val
115 120 125
Trp Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His
130 135 140
Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145 150 155 160
Val Gly Asp Pro Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
165 170 175
Pro Ala Arg Lys Glu Tyr Ile Lys Asn Phe Leu Arg Glu Glu Gly Gly
180 185 190
Gly Gln Ala Val Asp Ala Ala Ala
195 200

<210> 13
<211> 920
<212> DNA
<213> Human

<220>
<221> CDS
<222> (1) .. (564)

<400> 13

cga aca cgg cac ccg cac tgc gcg tca gtg gtg cag gcc tgg tat atg	48
Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met	
1 5 10 15	
gac gac gcc ccg ggc acc cgc ggc aac ccc acc gcc ccg acc ccg gcc	96
Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala	
20 25 30	
gcc cag tgc gct gga gca gct gcg cgg ctc ggg gtg ctc tac tgg aag	144
Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys	
35 40 45	
ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga	192
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg	
50 55 60	
aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat	240
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp	
65 70 75 80	
aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat	288
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His	
85 90 95	
ttg cac ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac	336
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr	
100 105 110	
ttc gat gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag	384
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu	
115 120 125	
aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg	432
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr	
130 135 140	
gtg gac gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa	480
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu	
145 150 155 160	
ccg gtg tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc	528
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg	
165 170 175	
ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgtgcc	574
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala	
180 185	
tggaactaa cacgtgcctc gtaaaggtcc ccaatgtaat gaactgagca gaaaattcaa	634
tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga	694
ttatttgatc agaataatttt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga	754
gtcaccttca ttttctgtaa ctcaatcaag actggtgggt ccatggccct gtgttagttc	814
attgcattca gggtgagtc ccaatgaaag tttcatctcc cgaaatgcag ttccttagat	874
gcccatctgg acgtgaatgc cgcgcctgcg tgtaagaagg tgcaat	920

<210> 14
<211> 187
<212> PRT
<213> Human

<400> 14
Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
1 5 10 15
Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
20 25 30
Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
35 40 45
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
50 55 60
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
65 70 75 80
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
85 90 95
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
100 105 110
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
115 120 125
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
130 135 140
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
145 150 155 160
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
165 170 175
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

<210> 15
<211> 972
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (17)..(556)

<400> 15
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Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
1 5 10
gac ccg cgg aag ccc cac cgc gca cag ccc gac cgc ccc gtg agc ctg 100
Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
15 20 25
gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac 148
Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
30 35 40
aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac 196
Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
45 50 55 60
tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat 244
Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn

65	70	75	
tac gag gag aag atc aag atg ttc ttt	gag gaa cat ctg cat ctg gat	292	
Tyr Glu Glu Lys Ile Lys Met Phe Phe	Glu Glu His Leu His Leu Asp		
80	85 90		
gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg	340		
Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg			
95	100 105		
gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg	388		
Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met			
110	115 120		
att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag	436		
Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys			
125	130 135 140		
aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca	484		
Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr			
145	150 155		
cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg	532		
Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met			
160	165 170		
agt ttt ttg gaa gga aca gca tag cagtgtcct caaagagaaa actgcactgt	586		
Ser Phe Leu Glu Gly Thr Ala			
175	180		
gtgaatctcc tgctgtggtg accgaatgga aagttgctca cttttctgct tttgtatttg	646		
aacttgaggc tagactagct ctctttgcta ggattgtgag atcagtgtct tttaaatgaa	706		
agcctctcta aaagtgagtt ttacatggaa gccacaaaaa tgtgaaaaag tgaccttaat	766		
tttccctaac tgtcaagact tagaggtata ggagccctgg attggtatgt gcattcatgc	826		
atggccaatc ttcattctccc agatcttttag gtgtctgttg gtgtgaagct atgcctcctg	886		
caagaggggca gttataacca gcacaactaa ccagatgacg tttttctcct ttgctgattg	946		
ttgagtgggg aagtgggggtt gttggt	972		

<210> 16
 <211> 179
 <212> PRT
 <213> Mouse

<400> 16
 Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala Asp Pro Arg Lys
 1 5 10 15
 Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu Glu Gln Leu Arg
 20 25 30
 Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn
 35 40 45
 Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn Tyr Ser Trp Met
 50 55 60
 Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn Tyr Glu Glu Lys
 65 70 75 80

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<210> 17
<211> 706
<212> DNA
<213> Zebrafish

<220>
<221> CDS
<222> (36)..(581)
<223> n at positions 634 and 642 is unknown
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<400> 17																
gtactgcgca tggagaccga accggactgt tcaag atg agt gtt ttc gag gca																
Met Ser Val Phe Glu Ala																
1 5																
53																
tgg tac atg gat gaa gag tcc gga gag gac cag aga ctc ccg cac aaa																
Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys																
10 15 20																
101																
ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga																
Leu Ser Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly																
25 30 35																
149																
gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa																
Val Phe His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu																
40 45 50																
197																
ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata																
Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile																
55 60 65 70																
245																
acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg																
Thr Ile His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met																
75 80 85																
293																
ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg																
Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu																
90 95 100																
341																
gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc																
Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile																
105 110 115																
389																

cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att 437
Arg Ile Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
120 125 130

tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt 485
Tyr His Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
135 140 145 150

ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat 533
Leu Phe Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
155 160 165

gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga 581
Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
170 175 180

aatgcctgat gggattgatt tagtgctgag aatcagactc tgcgggtgcct tanacagaca 641

ngcagcaata gtagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag 701

attat 706

<210> 18

<211> 181

<212> PRT

<213> Zebrafish

<223> n at positions 634 and 642 is unknown

<400> 18

Met Ser Val Phe Glu Ala Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp
1 5 10 15
Gln Arg Leu Pro His Lys Leu Ser Pro Asn Gln Pro Val Ser Val Gln
20 25 30
Gln Leu Glu His Ile Gly Val Phe His Trp Lys Leu Asn Ala Asp Ile
35 40 45
Tyr Glu Asn Asp Pro Glu Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr
50 55 60
Ser Phe Met Asp Ile Ile Thr Ile His Pro Asp Lys Leu Pro Asp Tyr
65 70 75 80
Gln Asn Lys Leu Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp
85 90 95
Glu Ile Arg Tyr Ile Leu Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp
100 105 110
Glu Gly Asp Arg Trp Ile Arg Ile Ala Val Ser Lys Gly Asp Leu Ile
115 120 125
Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Ser Asn
130 135 140
Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Lys Ala
145 150 155 160
Tyr Asn Arg Pro Ala Asp Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn
165 170 175
Ser Leu Gly Ser Ser
180